

Application No.: 09/677,752
Amendment Dated: February 17, 2006
Reply to Office Action of: August 30, 2005

Attorney Docket No.: 71515.087.999
Customer No.: 35161

REMARKS

This Amendment is in response to the Office Action mailed on August 30, 2005, for the present application, which has been reviewed. Considered together with the following remarks, the arguments below and request for reconsideration are believed sufficient to place the application into condition for allowance. No new matter has been added to the application. Applicants express appreciation for the thoughtful examination by the Examiner.

Support for the amendments can be found in the specification as follows:

Amendment to claim 108:	page 18, Table 1.
Amendment to claim 130:	page 21, lines 20-34.

The present invention is drawn to PMP polypeptides of *Chlamydia*, further defined by amino acid and nucleotide sequences thereof, used in vaccine formulations comprising an effective amount of said polypeptide.

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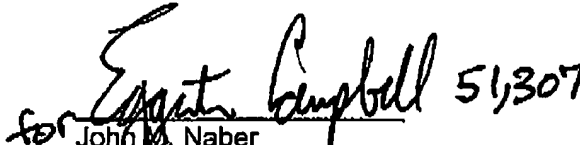
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CONCLUSION

In light of the foregoing, Applicants respectfully submit they have addressed each and every item presented by the Examiner in this Office Action. Favorable reconsideration of all of the claims as amended is earnestly solicited. Applicants submit that the present application, with the foregoing claim and specification amendments and accompanying remarks, is in a condition for allowance and respectfully request such allowance.

In the event any further matters requiring attention are noted by Examiner or in the event that prosecution of this application can otherwise be advanced thereby, a telephone call to Applicants' undersigned representative at the number shown below is invited.

Respectfully submitted,


for John M. Naber 51307
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DC 71515-07 108702v2 2/17/2006

Thursday, September 8, 2001

Blast Result

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Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix: BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☒ Align

Sequence 1 k|seq_1 Length 956 (1..956)

Sequence 2 k|seq_2 Length 965 (1..965)



Score and expect value) is calculated based on the size of nr database

Score = 1885 bits (4884), Expect = 0.0
Identities = 925/934 (99%), Positives = 930/934 (99%)

Query: 23 VPDPTKESLSNKISLTGDTNHLTNCYLDNLRILAILQKTPNEGAAVTITDYLSPFDQK 82
VDPPTKESLSNKISLTGDTNHLTNCYLDNLRILAILQKTPNEGAAVTITDYLSPFDQK
Sbjct: 32 VPDPTKESLSNKISLTGDTNHLTNCYLDNLRILAILQKTPNEGAAVTITDYLSPFDQK 91

Query: 83 EGIYFAKNLTPESGGAIGYASPNSTVEIRDITIGPVIFENNTCCRPFTSSNPNAAVVKIR 142
EGYFAKNLTPESGGAIGYASPNSTVEIRDITIGPVIFENNTCCRPFTSSNPNAAVVKIR
Sbjct: 92 EGIYFAKNLTPESGGAIGYASPNSTVEIRDITIGPVIFENNTCCRPFTSSNPNAAVVKIR 151

Query: 143 EGGAIHAQNLYINHHNDVVGFMKNFSYVRGGAISTANTFVVSQSCFLFMDNICIQNT 202
EGGAIHAQNLYINHHNDVVGFMKNFSYVRGGAISTANTFVVSQSCFLFMDNICIQNT
Sbjct: 152 EGGAIHAQNLYINHHNDVVGFMKNFSYVRGGAISTANTFVVSQSCFLFMDNICIQNT 211

Query: 203 AGKGGAIYAOTNSFSFNCDLFFINNACCAGGAI FSPICSLTGNRGNI VYNNRCFQIV 262
AGKGGAIYAOTNSFSFNCDLFFINNACCAGGAI FSPICSLTGNRGNI VYNNRCFQIV
Sbjct: 212 AGKGGAIYAOTNSFSFNCDLFFINNACCAGGAI FSPICSLTGNRGNI VYNNRCFQIV 271

Query: 263 ETASSEASDGGAIKVTRLDTGNRGRIFSDNITKNYGGAIYAPVVTLVNQGPTYPINN 322
ETASSEASDGGAIKVTRLDTGNRGRIFSDNITKNYGGAIYAPVVTLVNQGPTYPINN
Sbjct: 272 ETASSEASDGGAIKVTRLDTGNRGRIFSDNITKNYGGAIYAPVVTLVNQGPTYPINN 331

Query: 323 VANKGGAIYIDGTNSKISADRHAIIFNENIVTNVTANOTSTSANPPRNNAITVASS 382
+ANKGGAIYIDGTNSKISADRHAIIFNENIVTNVTANOTSTSANPPRNNAITVASS
Sbjct: 332 IANKGGAIYIDGTNSKISADRHAIIFNENIVTNVTANOTSTSANPPRNNAITVASS 391

Query: 383 GEILLGAGSSQNLIFYDPIEVSNAGVSVPNKEADQTGVSVPFGATVNSADPHQRNLQTK 442
GEILLGAGSSQNLIFYDPIEVSNAGVSVPNKEADQTGVSVPFGATVNSADPHQRNLQTK
Sbjct: 392 GEILLGAGSSQNLIFYDPIEVSNAGVSVPNKEADQTGVSVPFGATVNSADPHQRNLQTK 451

Query: 443 TPAPLTLENGFLCIEDHAQLTVNRFTQTGGVSLNGAVLSCYKNGAGNSASNASITLKH 502
TPAPLTLENGFLCIEDHAQLTVNRFTQTGGVSLNGAVLSCYKNGAGNSASNASITLKH
Sbjct: 452 TPAPLTLENGFLCIEDHAQLTVNRFTQTGGVSLNGAVLSCYKNGAGNSASNASITLKH 511

Query: 503 IGLKSSILKSGAEIPLMVEPTNENNYTADTAATFSLSDVKLSLIDYGNSPYESTDL 562
IGLKSSILKSGAEIPLMVEPTNENNYTADTAATFSLSDVKLSLIDYGNSPYESTDL

day, September 6, 2001

Blast Result

Page: 2

Query: 512 IGLNLSSILKSGAEIPLWVEPTNNSNNTADTAATFSLSDVKLSLIDYGNSPYESTDL 571
Query: 563 THALSSQPMLSISEASDNQLRSDDMDFSGLNVPHYGQGLNSWGWAKTQDPEPASSATIT 622
THALSSQPMLSISEASDNQLRSDDMDFSGLNVPHYGQGLNSWGWAKTQDPEPASSATIT 622
Query: 572 THALSSQPMLSISEASDNQLRSDDMDFSGLNVPHYGQGLNSWGWAKTQDPEPASSATIT 631
Query: 623 DPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTFSDHFF 682
DPK+KANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTFSDHFF 682
Query: 632 DPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTFSDHFF 691
Query: 693 WGITGGGLGMNVYQEPRENHPGFHRSSTGYAGMIAGQTHTFSLKFSQTYTKLNERYAKN 742
WGITGGGLGMNVYQEPRENHPGFHRSSTGYAGMIAGQTHTFSLKFSQTYTKLNERYAKN 742
Query: 692 WGITGGGLGMNVYQEPRENHPGFHRSSTGYAGMIAGQTHTFSLKFSQTYTKLNERYAKN 751
Query: 743 NVSSKNYSQCGEMLFSLQEGFLLAKLVGLYSYGDHNCHEFYTQGENLTSQGTFRSQTMGG 802
NVSSKNYSQCGEMLFSLQEGFLLAKLVGLYSYGDHNCHEFYTQGENLTSQGTFRSQTMGG 802
Query: 752 NVSSKNYSQCGEMLFSLQEGFLLAKLVGLYSYGDHNCHEFYTQGENLTSQGTFRSQTMGG 811
Query: 803 AVFFDLPMKPFQSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVK 862
AVFFDLPMKPFQSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVK 862
Query: 812 AVFFDLPMKPFQSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVK 871
Query: 863 GSFNATQRPQAWTVELAYQPVLYRQELEIATQLLASKGIWFGSGSPSSRHMSYKISQQ 922
GSFNATQRPQAWTVELAYQPVLYRQE IATQLLASKGIWFGSGSGSPSSRHMSYKISQQ 922
Query: 872 GSFNATQRPQAWTVELAYQPVLYRQEPGIATQLLASKGIWFGSGSGSPSSRHMSYKISQQ 931
Query: 923 TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF 956
TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF 956
Query: 932 TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF 965

PU time: 0.36 user secs. 0.02 sys. secs 0.38 total secs.

apped
ambda K H
0.316 0.132 0.396

apped
ambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 12,524
Number of Sequences: 0
Number of extensions: 873
Number of successful extensions: 15
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
Length of query: 956
Length of database: 239,316,239
Effective HSP length: 131
Effective length of query: 825
Effective length of database: 206,523,009
Effective search space: 170381482425
Effective search space used: 170381482425
r: 9
k: 40
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.6 bits)
S2: 77 (34.3 bits)